

copy of alignment to App.

AAD07974

ID AAD07974 standard; cDNA; 1957 BP.

XX

DE Rice cysteinyl-tRNA synthetase cDNA clone rs11n.pk016.p18.

OS Oryza sativa.

XX

PN US6255090-B1. PARENT App.

XX

PA (DUPO) DU PONT DE NEMOURS & CO E I.

PA (PION-) PIONEER HI-BRED INT INC.

XX

PI Famodu LO, Orozco EM, Rafalski JA;

XX

SQ Sequence 1957 BP; 599 A; 384 C; 470 G; 504 T; 0 other;

Alignment Scores:

Pred. No.:	1.3e-194	Length:	1957
Score:	2398.00	Matches:	452
Percent Similarity:	91.47%	Conservative:	41
Best Local Similarity:	83.86%	Mismatches:	38
Query Match:	76.42%	Indels:	8
DB:	22	Gaps:	3

US-09-846-589A-10 (1-599) x AAD07974 (1-1957)

CORN Qy Seq 10 57 SerProProSerAlaThrIleAlaGluAlaThrAlaPro---ProGlnLeuLeuLeuPhe 75
Db 45 TCCCCCTCCGCTCTCACGATGGCGGAGAGCGCGAACGCCAGCCGCAGCTGGAGCTCTTC 104

Qy 76 AsnSerPheThrLysArgGluGluProPheGlnProArgValGluGlyLysValGlyMet 95
Db 105 AACTCGATGACGAAGAAGAAGGAGCTCTCGAGCCGCTTGTGGAGGGGAAGGTCCGCATG 164

Qy 96 TyrValCysGlyValThrProTyrAspPheSerHisIleGlyHisAlaArgAlaTyrVal 115
Db 165 TATGTGTGCGCGTCACGCCCTACGACTTCAGCCACATCGGCCACGCCGCCTACGTC 224

Qy 116 AlaPheAspValLeuTyrArgTyrLeuLysPheLeuGlyTyrGluValGluTyrValArg 135
Db 225 GCCTTCGACGTCTCTACAGGTATCTTAAATTCTGGGTACGAGGTCAATATGTGCGC 284

Qy 136 AsnPheThrAspIleAspAspLysIleIleLysArgAlaAsnGluArgGlyGluThrVal 155
Db 285 AACTTCACTGATATTGATGACAAGATTATCAAACGAGCAAATGAAGCTGGTAAACTGTA 344

Qy 156 ThrSerLeuSerSerGlnPheIleAsnGluPheLeuAspMetThrGluLeuGlnCys 175
Db 345 ACTAGCTTGAGCAGCCGGTTATTAAATGAATTCTCTCGATATGGCTCAGCTCCAGTGC 404

Qy 176 LeuProProThrCysGluProArgValThrGluHisIleGluHisIleIleLysLeuIle 195
Db 405 TTACCCCCAACTTGTGAGCCACGTGTGACGGATCACATTGAACATATTATAGAGTTGATA 464

Qy 196 ThrGlnIleMetGluAsnGlyLysAlaTyrAlaIleGluGlyAspValTyrPheSerVal 215
Db 465 ACCAAGATAATGGAGAATGGGAAAGCCTATGCTATGGAAGGAGATGTTACTTTCAAGTT 524

Qy	216	GluSerPheProGluTyrLeuSerLeuSerGlyArgLysPheAspGlnAsnGlnAlaGly	235
	::::::::::		
Db	525	GATACTTCCCTGAGTATCTCAGTTATCTGGAAGGAAGTTAGATCATAATCTGCTGGT	584
Qy	236	AlaArgValAlaPheAspThrArgLysArgAsnProAlaAspPheAlaLeuTrpLysAla	255
	::::::::::		
Db	585	TCGCGGGTTGCTGTCGATACAAGAAAGCGGAACCTGCAAGACTTGCAGCTGTGGAAGGCT	644
Qy	256	AlaLysGluGlyGluProPheTrpAspSerProTrpGlyArgGlyArgProGlyTrpHis	275
Db	645	GCTAAGGAAGCGAACCTTCTGGGATAGCCCATGGGGCGTGGTAGACCAGGATGGCAT	704
Qy	276	IleGluCysSerAlaMetSerAlaHisTyrLeuGlyHisValPheAspIleHisGlyGly	295
Db	705	ATTGAATGCAGTGCAATGAGTGCTCATTATTAGGACATGTGTTGATATCCATGGTGGA	764
Qy	296	GlyLysAspLeuIlePheProHisHisGluAsnGluLeuAlaGlnSerArgAlaAlaTyr	315
Db	765	GGGAAAGATCTGATATTCCCTCATCATGAGAATGAGCTTGCTCAGAGCCGGCAGCTTAT	824
Qy	316	ProAspSerGluValLysCysTrpMetHisAsnGlyPheValAsnLysAspAspLysLys	335
	::		::
Db	825	CCAGAAAGATGAGGTCAAATGTTGGATGCACAATGGGTTGTTAACAAAGGATGATCAGAAA	884
Qy	336	MetAlaLysSerAspAsnAsnPhePheThrIleArgAspIleIleAlaLeuTyrHisPro	355
	::		
Db	885	ATGTCAAAGTCAGATAAAAATTCTTCACAATCCGAGATATTATTGATCTGTACCATCCC	944
Qy	356	MetAlaLeuArgPhePheLeuMetArgThrHisTyrArgSerAspValAsnHisSerAsp	375
Db	945	ATGGCTTGAGGTTTCCTGATGCGCACACATTACAGAGGAGATGTGAATCACTCTGAC	1004
Qy	376	GlnAlaLeuGluIleAlaSerAspArgValTyrTyrIleTyrGlnThrLeuTyrAspCys	395
	::::		
Db	1005	AAAGCACTTGAGATAGCATCTGATCGTGTCTACTACATATATCAGACTTATATGACTGT	1064
Qy	396	GluGluValLeuAlaThrTyrArgGluGluGlyThrSerLeuProValProSerGluGlu	415
			::
Db	1065	GAGGAAGTGTGCTCAATATCGTGGAGAGAATATCTCTGTCCCGGTCCTGTTGAGGAA	1124
Qy	416	GlnAsnLeuIleGlyLysHisHisSerGluPheLeuLysHisMetSerAsnAspLeuLys	435
	::		::
Db	1125	CAAGATATGGTTAACAAAGCACCATTAGAATTCTTGGAACTATGGCGGATGATCTTAGA	1184
Qy	436	ThrThrAspValLeuAspArgCysPheMetGluLeuLeuLysAlaIleAsnSerSerLeu	455
			::
Db	1185	ACAACAGATGTTCTGGATGGC---TTTACTGACTGCTGAAGGCAATTACAGCAATTG	1241
Qy	456	AsnAspLeuLysLysLeuGlnGlnLysIleGluGlnGlnLysLysGlnGlnGlnGln	475
Db	1242	AATGATTAAAGAAGTTGCAACAGAAGCTAGAGCAGCAAAAG-----	1283
Qy	476	LysLysGlnGlnGlnLysGlnGlnGlnGlnLysGlnGlnLeuGlnLysGlnPro	495
Db	1284	AAGAAACAACAAACAGCAGAAGCAGCAGCAGCAGGACAGAAACAAACCA	1343

Qy 496 GluAspTyrIleGlnAlaLeuIleAlaLeuGluThrGluLeuLysAsnLysLeuSerIle 515
|||:::|||||||:::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 1344 GAAGAATATATTCAAGCTATGTTGCACTTGAGACAGAAATTAAAAATAAAATATCTATC 1403

Qy 516 LeuGlyLeuMetProSerSerLeuAlaGluValLeuLysGlnLeuLysAspLysSer 535
|||||:|||||:|||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1404 CTTGGTCTGATGCCACCTTCTCCTGGCAGAGGCAGTGAAGCAACTTAAGGATAAAGCT 1463

Qy 536 LeuLysArgAlaGlyLeuThrGluGluGlnLeuGlnGluGlnIleGluGlnArgAsnVal 555
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1464 TTGAAGAGAGCAGGGTTGACTGAAGAACTGTTGCAGGAGCAAATTGAGCAGAGAACTGCT 1523

Qy 556 AlaArgLysAsnLysGlnPheGluIleSerAspGlyIleArgLysAsnLeuAlaThrLys 575
|||||:|||||:|||||:|||||:|||||:|||||:|||:|||:
Db 1524 GCAAGGAAAACAAGCAGTTGATGTCTGACCAAATCAGGAAACAGCTAGGCAGCAAA 1583

Qy 576 GlyIleAlaLeuMetAspGluProSerGlyThrValTrpArgProCysGluProGlu 594
|||||:|||||:|||||:|||||:|||||:
Db 1584 GGCATAGCCCTCATGGATGAACCTACTGGTACAGTATGGAGACCATGCGAGCCAGAG 1640



copy of alignment to Applicant

AAD07975

ID AAD07975 standard; cDNA; 2183 BP.

XX DE Soybean cysteinyl-tRNA synthetase cDNA clone sf11.pk0013.f9.
XX OS Glycine max.

XX PN US6255090-B1.

PA PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX (PION-) PIONEER HI-BRED INT INC.

PI XX Famodu LO, Orozco EM, Rafalski JA;

SQ Sequence 2183 BP; 621 A; 411 C; 485 G; 666 T; 0 other;

Alignment Scores:

Pred. No.:

Score: 1.79e-115

Percent Similarity: 1470.00

Best Local Similarity: 65.65%

Query Match: 51.19%

DB: 46.85%

22

Length: 2183

Matches: 301

Conservative: 85

Mismatches: 146

Indels: 57

Gaps: 8

US-09-846-589A-10 (1-599) x AAD07975 (1-2183)

Qy

7 SerThrThrProLeuSerProProProProProGlnIleProPheArgValCysLeu 26
||| ||||||||| ||| |||||
115 TCCCTCACTCCGCTCCACCCAGACTCCACCGCCGCCA-----

Qy 27 AlaSerGlyAlaSerArgLeuAlaArgAlaThrThrMetAlaGluGluValGlnAlaPro 46
:::||||||| ||||| :::: |||||

Db 151 TCTTCAGGAGCAAAACTTTCTTTGCGGCC-ACCTCGTCC-----CCGCCG 197
||| ||| :::: |||||

Qy 47 LeuSerAlaThrMetAlaLysGluAlaGlnSerProProSerAlaThrIleAlaGluAla 66
|||::: ||||| :::: |||||

Db 198 TTGACG-----GCGGAGAAGGGTTGCGGCCAAATCCGACGCCGAGTGT 239
|||::: :::: |||||

Qy 67 ThrAlaProProGlnLeuLeuLeuPheAsnSerPheThrLysArgGluGluProPheGln 86
|||:::||| ||||| ::::: ::::||| |||:::

Db 240 CCCACCTTGCCGGAGGTGTGGCTGCACAAACACCATGAGTAGGACGAAGGAACCTTCAA 299
|||:::||| ||||| ::::: ::::||| |||:::

Qy 87 ProArgValGluGlyLysValGlyMetTyrValCysGlyValThrProTyrAspPheSer 106
|||:::||| ||||| ::::: ||||| ::::: ||||| |||:::

Db 300 CCCAAAGTGGAATCCAAAGTGGGAATGTACGTGTGCGCGTCACCGCTTATGATCTTAGC 359
|||:::||| ||||| ::::: ||||| ::::: ||||| |||:::

Qy 107 HisIleGlyHisAlaArgAlaTyrValAlaPheAspValLeuTyrArgTyrLeuLysPhe 126
|||||:::||| ||||| ::::: ||||| ::::: ||||| ::::: |||||

Db 360 CATATTGGACACGCTCGCTATACGTCAATTGACCTTCTTACAGATACTTTAAGCAT 419
|||||:::||| ||||| ::::: ||||| ::::: ||||| ::::: |||||

Qy 127 LeuGlyTyrGluValGluTyrValArgAsnPheThrAspIleAspAspLysIleIleLys 146
|||||:::||| ||||| ::::: ||||| ::::: ||||| ::::: |||||

Db 420 TTGGGATTGAAAGTCTGTTATGTTGCAATTCACTGACGTAGATGACAAGATAATTGCT 479
|||||:::||| ||||| ::::: ||||| ::::: ||||| ::::: |||||

Qy 147 ArgAlaAsnGluArgGlyGluThrValSerLeuSerSerGlnPheIleAsnGluPhe 166
||||| ||| ||||| ::::: ||||| ::::: ||||| ::::: |||||

Db 480 AGAGCAAAGGAGTTAGGAGAAGATCCAATCAGTTGAGCTGGCGCTATTGTGAAGAGTTC 539
||||| ||| ||||| ::::: ||||| ::::: ||||| ::::: |||||

Seq 9
CORN

soybean

Qy 167 LeuLeuAspMetThrGluLeuGlnCysLeuProProThrCysGluProArgValThrGlu 186
 ||||| |||| ||||| ||||::: ||||||:::|||:::|||
 Db 540 TGTCAAGACATGGTAACCTTAATTGTCTGTCTCCCTCTGTGGAACCAAAGGTCTCAGAG 599

 Qy 187 HisIleGluHisIleIleLysLeuIleThrGlnIleMetGluAsnGlyLysAlaTyrAla 206
 |||::: ||||| ::||| ::|||::: ||||| |||||
 Db 600 CACATGCCCAAATCATTGATATGATTGAGAAGATCCTAATAATGGGTATGCCTACATT 659

 Qy 207 IleGluGlyAspValTyrPheSerValGluSerPheProGluTyrLeuSerLeuSerGly 226
 :::::::||||| |||||:::||| ||||||| |||||
 Db 660 GTTGATGGGATGTGTACTTTAATGTAGAAAAATTCCAGAATATGGAAACTATCTAGT 719

 Qy 227 ArgLysPheAspGlnAsnGlnAlaGlyAlaArgValAlaPheAspThrArgLysArgAsn 246
 ||| :: |||:::||| ||| ||||| |||:::|||:::|||
 Db 720 CGAGATCTAGAAGATAATCGAGCTGGTGGAGAGGGTTGCAGTTGATTCTAGAAAGAAAAAT 779

 Qy 247 ProAlaAspPheAlaLeuTrpLysAlaAlaLysGluGlyGluProPheTrpAspSerPro 266
 ||||||| |||||:::||| ||||| ||||| |||||:::|||
 Db 780 CCTGCTGATTTGCTCTTGGAAAGTCTGCAAAGCCAGGGAGCCATTGGGAGAGTCCC 839

 Qy 267 TrpGlyArgGlyArgProGlyTrpHisIleGluCysSerAlaMetSerAlaHisTyrLeu 286
 ||||| ||||||| ||||| ||||| ||||| |||||
 Db 840 TGGGGTCCTGGAAGACCTGGGTGGCATATTGAATGCAGTGCATGAGTGCAGCTATCTT 899

 Qy 287 GlyHisValPheAspIleHisGlyGlyLysAspLeuIlePheProHisHisGluAsn 306
 |||::: ||||||| ||||| |||||:::||| |||||
 Db 900 GGTTACTCTTTGATATCCATGGTGGAGGAATCGACCTTGTGTTCCCTACCATGAGAAT 959

 Qy 307 GluLeuAlaGlnSerArgAlaAlaTyrProAspSerGluValLysCysTrpMetHisAsn 326
 |||:::||||| ||||| |||:::||| |||||
 Db 960 GAAATTGCTCAGAGTTGTGCTGCATGTAAGAAAAGTGTATAAGTATATGGATGCACAAT 1019

 Qy 327 GlyPheValAsnLysAspAspLysMetAlaLysSerAspAsnAsnPhePheThrIle 346
 ||||| ||||| ||| |||||:::||| |||||
 Db 1020 GGTTTGTCACCATTGACTCTGTGAAATGTCAAATCTTGGGAATTTCACAATA 1079

 Qy 347 ArgAspIleIleAlaLeuTyrHisProMetAlaLeuArgPhePheLeuMetArgThrHis 366
 ||| ::||| ::|||:::|||:::||| |||||
 Db 1080 CGTCAGGTTATAGACGTTACCATCCACTGGCCTTGAGATATTTTGATGAGCGCACAT 1139

 Qy 367 TyrArgSerAspValAsnHisSerAspGlnAlaLeuGluIleAlaSerAspArgValTyr 386
 ||||||| ::|||:::|||::: ||||| ||||| |||||
 Db 1140 TATCGATCTCCTATTAACTACTCAAATACAGCTCGAAAGTGTGTTCAAGACCGTGT 1199

 Qy 387 TyrIleTyrGlnThrLeuTyrAspCysGluGluValLeuAlaThrTyrArgGluGluGly 406
 |||||||:::|||:::|||::: ||||| ||| :: ::
 Db 1200 TATATATATGAGACATTACATGAATGTGAAAGCTTTGAATCAGCATGATCAGAGGAAG 1259

 Qy 407 ThrSerLeuProValProSerGluGluGlnAsnLeuIleGlyLysHisSerGluPhe 426
 ||| ||| :: :::::||| ||| ||| |||
 Db 1260 GATTCC-----ACCCCACCGGATACTTGGATATTATTGATAAGTCCACGATGTTTT 1313

 Qy 427 LeuLysHisMetSerAsnAspLeuLysThrThrAspValLeuAspArgCysPheMetGlu 446
 ||| |||||:::|||::: ||| |||
 Db 1314 TTGACCTCAATGTCGGATGATCTCACACTCCAGTTGTATTG----- 1355

Qy 447 LeuLeuLysAlaIleAsnSerSerLeuAsnAsp---LeuLysLysLeuGlnGlnLysIle 465
 ::: :::::::||| ||||| :::: :::
Db 1356 -----GCTGGAATGTCTGATCCATTAAATCAATCAATGATTGCTG 1397

Qy 466 GluGlnGlnLysLysLysGlnGlnGlnLysLysGlnGlnGlnLysGlnGlnGln 485
 :::||| |||:::|||||| :::
Db 1398 CATGCTCGTAAGGGGAAAAACAAACAATTTCGA----- 1430

Qy 486 GlnLysGlnGlnGlnLeuGlnLysGlnProGluAspTyrIleGlnAlaLeuIleAlaLeu 505
 ||||:::::||| |||||
Db 1431 -----ATCGAATCACTATCAGCTTG 1451

Qy 506 GluThrGluLeuLysAsnLysLeuSerIleLeuGlyLeuMetProSerSerSerLeuAla 525
 ||| ::::::: |||:::::||||||| ||||| ::::||| :::
Db 1452 GAGAAGAGCGTCAGGGATGTCCTTACTGTTTAGGACTTATGCCT---GCAAGTTACTCT 1508

Qy 526 GluValLeuLysGlnLeuLysAspLysSerLeuLysArgAlaGlyLeuThrGluGln 545
 |||||||:::||||||| |||:::||||||| ||||| |||||:::
Db 1509 GAGGTTTGCAGCAGCTTAAGGTAAAAGCTTAAAACGTGCAAACTTACGGAAGAAGAA 1568

Qy 546 LeuGlnGluGlnIleGluGlnArgAsnValAlaArgLysAsnLysGlnPheGluIleSer 565
 ::: ::::::| |||||:::||| ||||| |||::::: |||
Db 1569 GTCTTGAGAAAATTGAAGAACGGGCTACTGCTAGAATGCAAAGGAGTATGCTAAATCG 1628

Qy 566 AspGlyIleArgLysAsnLeuAlaThrLysGlyIleAlaLeuMetAspGluProSerGly 585
 ||| |||||:::||| ||||| ||||| ||||| |||||:::|||
Db 1629 GATGCAATCAGGAAGGATTGGCTGTACTGGTATTACTCTTATGGACAGTCCAAATGGC 1688

Qy 586 ThrValTrpArgProCysGluPro 593
 ||| ||||| ||| |||
Db 1689 ACAACTTGGAGGCCCTGCCATTCCCT 1712

